OIPE

RAW SEQUENCE LISTING   DATE: 01/16/2001
PATENT APPLICATION: US/09/748,451   TIME: 11:52:45

          Input Set : A:\UTSD546USD1.txt
          Output Set: N:\CRF3\01162001\I748451.raw

    3 <110> APPLICANT: WANG, XIAODONG
    4   LIU, XUESONG
    6 <120> TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
    8 <130> FILE REFERENCE: UTSD:546USD1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/748,451
   11 <141> CURRENT FILING DATE: 2000-12-22
   13 <150> PRIOR APPLICATION NUMBER: 09/061,702
   14 <151> PRIOR FILING DATE: 1998-04-16
   16 <160> NUMBER OF SEQ ID NOS: 21
   18 <170> SOFTWARE: PatentIn Ver. 2.1
   20 <210> SEQ ID NO: 1
   21 <211> LENGTH: 2839
   22 <212> TYPE: DNA
   23 <213> ORGANISM: Homo sapiens
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   28 ggacatctgc aatgctccag aagcccaaga gcgtgaagct gcgggccctg cgcagcccga 180
   29 ggaagttcgg cgtggctggc cggagctgcc aggaggtgct gcgcaagggc tgtctccgct 240
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   31 aagattactt ccccagtgtt cccgacaacg ccgagctggt gctgctcacc ttgggccagg 360
   32 cctggcaggg ctatgtgagc gacatcaggc gcttcctcag tgcatttcac gagccacagg 420
   33 tggggctcat ccaggccgcc cagcagctgc tgtgtgatga gcaggcccca cagaggcaga 480
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   37 cagtgggtgc ggaggctcag gaggaattcc tgcgggtcct cggctccatg tgccagaggc 720
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   39 tctgcacacc ggaaggctgg ttctcctgcc agggtccctt gacatggac agctgcttat 840
   40 caagacactc catcaacccc tacagtaaca gggagagcag gatcctcttc agcacctgga 900
   41 acctggatca cataatagaa aagaaacgca ccatcattcc tacactggtg gaagcaatta 960
   42 aggaacaaga tggaagagaa gtggactggg agtattttta tggcctgctt tttacctcag 1020
   43 agaacctaaa actagtgcac attgtctgcc ataagaaaac cacccacaag ctcaactgtg 1080
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   45 gccagtgaca cgtacacacc acgtcctggt ctttgtttga ggcctgacgt gggcatcatt 1200
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60 atcttggctc actgcaacct ccgcctctca ggttcaagtg gttctcctgc ctcagcctcc 2100
61 caagtagctg ggattacagg cacctaccac cagggccagc taatttttgt atgtttagta 2160
62 gtaacggggt ttcaccatgt tggccaggct gttctcgaac tcctgacctc aggtgatctg 2220
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70 gatacggggg ttgggctaga ttacagaggg ctcattttct acgtcatgta ttttatgata 2700
71 cttgaatttt ttgaaatggg catttatttt ataacatgtt aaaatgtact ttttaaatta 2760
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77 <211> LENGTH: 338
78 <212> TYPE: PRT
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86             20                  25                  30
88 Gly Cys Leu Arg Phe Gln Leu Pro Glu Arg Gly Ser Arg Leu Cys Leu
89         35                  40                  45
91 Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro
92     50                  55                  60
94 Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly
95 65                  70                  75                  80
97 Tyr Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln
98             85                  90                  95
100 Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala
101             100                 105                 110
103 Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln
104             115                 120                 125
106 Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly
107     130                 135                 140
109 Leu Glu Ser Arg Phe Gln Ser Lys Ser Gly Tyr Leu Arg Tyr Ser Cys
110 145                 150                 155                 160
112 Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser
113             165                 170                 175
115 Thr Val Gly Ala Glu Ala Gln Glu Glu Phe Leu Arg Val Leu Gly Ser
116             180                 185                 190
118 Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp
119             195                 200                 205
121 Arg Gly Ala Lys Gly Gly Ser Arg Leu Cys Thr Pro Glu Gly Trp Phe
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130 Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu
131             260             265             270
133 Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr
134             275             280             285
136 Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile
137             290             295             300
139 Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg
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145 Arg Gln
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162                                                            Met Glu
163                                                              1
165 gtg acc ggg gac gcc ggg gta cca gaa tct ggc gag atc cgg act cta   166
166 Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg Thr Leu
167         5               10              15
169 aag ccg tgt ctg ctg cgc cgc aac tac agc cgc gaa cag cac ggc gtg   214
170 Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His Gly Val
171     20              25              30
173 gcc gcc tcc tgc ctc gaa gac ctg agg agc aag gcc tgt gac att ctg   262
174 Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp Ile Leu
175 35              40              45              50
177 gcc att gat aag tcc ctg aca cca gtc acc ctt gtc ctg gca gag gat   310
178 Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala Glu Asp
179             55              60              65
181 ggc acc ata gtg gat gat gac gat tac ttt ctg tgt cta cct tcc aat   358
182 Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro Ser Asn
183             70              75              80
185 act aag ttt gtg gca ttg gct agt aat gag aaa tgg gca tac aac aat   406
186 Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr Asn Asn
187         85              90              95
189 tca gat gga ggt aca gct tgg att tcc caa gag tcc ttt gat gta gat   454
190 Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp Val Asp
191         100             105             110
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194 Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala Arg Glu
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198 Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu Asp Leu
199                 135                 140                 145
201 cag atg ctt gtt gac gct ccc tgc tca gac ctg gct cag gaa cta cgt   598
202 Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu Leu Arg
203             150                 155                 160  .
205 cag agt tgt gcc acc gtc cag cgg ctg cag cac aca ctc caa cag gtg   646
206 Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln Gln Val
207       .  165                 170                 175
209 ctt gac caa aga gag gaa gtg cgt cag tcc aag cag ctc ctg cag ctg   694
210 Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu Gln Leu
211         180                 185                 190
213 tac ctc cag gct ttg gag aaa gag ggc agc ctc ttg tca aag cag gaa   742
214 Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys Gln Glu
215 195                 200                 205                 210
217 gag tcc aaa gct gcc ttt ggt gag gag gtg gat gca gta gac acg ggt   790
218 Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp Thr Gly
219                 215                 220                 225
221 atg agc aga gag acc tcc tcg gac gtt gcg ctg gcg agc cac atc ctt   838
222 Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His Ile Leu
223             230                 235                 240
225 act gca ctg agg gag aag cag gct cca gag ctg agc tta tct agt cag   886
226 Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser Ser Gln
227         245                 250                 255
229 gat ttg gag ttg gtt acc aag gaa gac ccc aaa gca ctg gct gtt gcc   934
230 Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala Val Ala
231     260                 265                 270
233 ttg aac tgg gac ata aag aag acg gag act gtt cag gag gcc tgt gag   982
234 Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala Cys Glu
235 275                 280                 285                 290
237 cgg gag ctc gcc ctg cgc ctg cag cag acg cag agc ttg cat tct ctc   1030
238 Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His Ser Leu
239             295                 300                 305
241 cgg agc atc tca gca agc aag gcc tca cca cct ggt gac ctg cag aat   1078
242 Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu Gln Asn
243             310                 315                 320
245 cct aag cga gcc aga cag gat ccc aca tagcagcagc gggaagtgtg        1125
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247         325                 330
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257 tgttcaaaag taattggcag tgattggcca ggcgcagtgg ctcacgcctg taatcccagc 1425
259 actgggaggc cgaggggggc ggatcgtgaa gtcaggagat cgagaccatc ctggctaaca 1485
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282 Gly Val Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp
283          35                  40                  45
285 Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala
286      50                  55                  60
288 Glu Asp Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro
289 65                  70                  75                  80
291 Ser Asn Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr
292              85                  90                  95
294 Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp
295              100                 105                 110
297 Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala
298          115                 120                 125
300 Arg Glu Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu
301      130                 135                 140
303 Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu
304 145                 150                 155                 160
306 Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln
307              165                 170                 175
309 Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu
310              180                 185                 190
312 Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys
313          195                 200                 205
315 Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp
316      210                 215                 220
318 Thr Gly Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His
319 225                 230                 235                 240
321 Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser
322              .245                 250                 255
324 Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala
325              260                 265                 270
327 Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala
328          275                 280                 285
330 Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His
331      290                 295                 300
333 Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu
334 305                 310                 315                 320
336 Gln Asn Pro Lys Arg Ala Arg Gln Asp Pro Thr
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 01/16/2001
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L:10 M:270 C: Current Application Number differs, Replaced Current Application
Number
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8